Table S1

	Off-target sequences	Position	Location	CFD scores	MIT scores	PCR oligo sequences 5’ > 3’
gRNA1:	**ATGACCATTTGTGCCCGAAT / TGG**	**chr4:43555934-43555856:+**	**Exon:Tln1**	**97**	**95**	
	AAGACCCTCTGTGCCCAAAT / CGG	chr2:174822060-174822082:+	Intergenic:Edn3-Gm14617	0.318935	0.25	F: ATGGTTGGTGCGAATAGGAAGTAGG R: GAATTAGCAGAAGTCGGCAGCTAGG
	ATGAACATTCATGCCCAAAT / CGG	chr17:69237876-69237898:+	Intron:Epb4.1l3	0.284444	0.30	F: GTGGCTTAGTTGTGGGTGAATCTCT R: GTTGAAACTGGTCAGTGAGTGTCAG
	GTGACCATTTCTGCCCAATT / AGG	chr2:119692094-119692116:+	Exon:Rtf1	0.215385	0.11	F: CATGAAGCAGATTCCCTTTGCATCC R: ACTAACGCTTGGCCCTTCTAAAACA
	ATGAGGGTTTGTGCCAGAAT / GGG	chr10:60359473-60359495:+	Intron:4632428N05Rik	0.211765	0.10	F: CCCAGAGAGAAACCTTATGGGTGAG R: AGAAATAGCAGTTTGCCGAGACAGG
	ATGCCCACTGGTGCCAGAAT / AGG	chr4:29493944-29493966:-	Intergenic:Gm11923-Gm11925	0.176471	0.24	F: GCTTTTACGGTGATACAGAAGAGCG R: CCATCCCAAATTGACTTTCCAAATGA
gRNA2:	**CTTACCAATTCGGGCACAAA / TGG**	**chr4:43555938-43555860:-**	**Exon:Tln1**	**97**	**90**	
	TTTAGAAATTCGGACACAAA / TGG	chr17:65378775-65378797:+	Intron:Tmem232	0.417857	0.14	F: CAGCTGTGAACCCTTATGCAAGTCA R: GGGAGGGTGCTTCTGAGTTAGTGGA
	GTTACTTATTCAGGCACAAA / TGG	chr1:61804468-61804490:-	Intron:4930448K12Rik	0.346196	0.29	F: TGCGTGACCTCTGTCATCACTGAAT R: TATGTCTGTAAGACTGCCCCCTCGT
	ATTACCAATTTGGGCACAAA / AGG	chr13:55268370-55268392:+	Intron:Nsd1	0.307692	4.79	F: CAGTCAGTGTAGTCCTTGGTTTTTGT R: GGAACTGATTTTACAACTGGCCCAA
	GTTAGCAAGTAGGGCACAAA / TGG	chr7:67494388-67494410:-	Intergenic:Mef2a-Lrrc28	0.254348	0.49	F: AAAGCCTCAACGATCCTCTTCTCTG R: GTCCTAAAGCACTGTCATCTGGTCG
	CTTACCAGTTAGGACACTAA / AGG	chr14:83619776-83619798:+	Intergenic:Gm24774-Pcdh17	0.20625	0.02	F: AGCAACAATGGCAAAATCAACATCCT R: ATCTCACTTCTGATCCCGGGTGTTA